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RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/722,441

DATE: 07/05/2003  
 TIME: 16:42:45

Input Set: A:\1533 1030002 seq list.txt  
 Output Set: N:\CRF3\07032001\I722441.raw

5 <110> APPLICANT: Hanke, Paul D.  
 7 Li-D'Elia, Lhing-Yew  
 9 Rayapati, John  
 11 Crafton, Corey  
 13 Walsh, Holly  
 17 <120> TITLE OF INVENTION: Increased Lysine Production by Gene Amplification  
 21 <130> FILE REFERENCE: 1533.1030002  
 25 <140> CURRENT APPLICATION NUMBER: 09/722,441  
 C--> 27 <141> CURRENT FILING DATE: 2001-06-22  
 30 <150> PRIOR APPLICATION NUMBER: US 60/173,707  
 31 <151> PRIOR FILING DATE: 1999-12-30  
 34 <150> PRIOR APPLICATION NUMBER: US 60/184,130  
 35 <151> PRIOR FILING DATE: 2000-02-22  
 39 <160> NUMBER OF SEQ ID NOS: 37  
 43 <170> SOFTWARE: PatentIn version 3.0  
 47 <210> SEQ ID NO: 1  
 49 <211> LENGTH: 1266  
 51 <212> TYPE: DNA  
 53 <213> ORGANISM: Corynebacterium glutamicum  
 57 <220> FEATURE:  
 59 <221> NAME/KEY: CDS  
 61 <222> LOCATION: (1)..(1266)  
 65 <400> SEQUENCE: 1  
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 68 1 5 10 15  
 70 gaa cgc att aga aac gtc gct gaa cgg atc gtt gcc acc aag aag gct 96  
 71 Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala  
 72 20 25 30  
 74 gga aat gat gtc gtg gtt gtc tgc tcc gca atg gga gac acc acg gat 144  
 75 Gly Asp Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp  
 76 35 40 45  
 78 gaa ctt cta gaa ctt gca gcg gca gtc aat ccc gtt ccg cca gtc cgt 192  
 79 Glu Leu Leu Glu Leu Ala Ala Val Asn Pro Val Pro Pro Ala Arg  
 80 50 55 60  
 82 gaa atg gat atg ctc ctg act gct ggt gag cgt att tct aac gct ctc 240  
 83 Glu Met Asp Met Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu  
 84 65 70 75 80  
 86 gtc gcc atg gct att gag tcc ctt ggc gca gaa gct caa tct ttc act 288  
 87 Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr  
 88 85 90 95  
 90 ggc tct cag gct ggt gtc acc acc gag ggc cac gga aac gca cgc 336  
 91 Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg  
 92 100 105 110  
 94 att gtt gac gtc aca ccc ggt cgt gtc cgt gaa gca ctc gat gag ggc 384  
 95 Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly  
 96 115 120 125

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99	Lys	Ile	Cys	Ile	Val	Ala	Gly	Phe	Gln	Gly	Val	Asn	Lys	Glu	Thr	Arg
100	130				135						140					
102	gat	gtc	acc	acg	tgg	ggg	cgt	ggg	tct	gac	acc	act	gca	gtt	gcg	480
103	Asp	Val	Thr	Thr	Leu	Gly	Arg	Gly	Gly	Ser	Asp	Thr	Thr	Ala	Val	Ala
104	145				150				155				160			
106	ttg	gca	gct	gtc	ttg	aac	gtc	gat	gtg	tgt	gag	att	tac	tcg	gac	gtt
107	Leu	Ala	Ala	Ala	Leu	Asn	Ala	Asp	Val	Cys	Glu	Ile	Tyr	Ser	Asp	Val
108									170				175			
110	gac	ggg	gtg	tat	acc	gct	gac	cgc	atc	gtt	cct	aat	gca	cag	aag	576
111	Asp	Gly	Val	Tyr	Thr	Ala	Asp	Pro	Arg	Ile	Val	Pro	Asn	Ala	Gln	Lys
112									185				190			
114	ctg	gaa	aag	ctc	atc	ttc	gaa	gaa	atc	tcg	gaa	ctt	gct	gct	gtt	624
115	Leu	Glu	Lys	Leu	Ser	Phe	Glu	Glu	Met	Leu	Glu	Leu	Ala	Ala	Val	Gly
116									195				200			
118	tcc	aag	att	ttg	gtg	ctg	cgc	agt	gtt	gaa	tac	gct	gtt	gca	ttc	aat
119	Ser	Lys	Ile	Leu	Val	Leu	Arg	Ser	Val	Glu	Tyr	Ala	Arg	Ala	Phe	Asn
120									215				220			
122	gtg	cca	ctt	cgc	gta	cgc	tcg	tct	tat	agt	aat	gat	ccc	ggc	act	ttg
123	Val	Pro	Leu	Arg	Val	Arg	Ser	Ser	Tyr	Ser	Asn	Asp	Pro	Gly	Thr	Leu
124	225					230				235			240			
126	att	gcc	ggc	tct	atg	gag	gat	att	cct	gtg	gaa	gaa	gca	gtc	ctt	acc
127	Ile	Ala	Gly	Ser	Met	Glu	Asp	Ile	Pro	Val	Glu	Glu	Ala	Val	Leu	Thr
128						245				250			255			
130	ggt	gtc	gca	acc	gac	aag	tcc	gaa	gcc	aaa	gta	acc	gtt	ctg	ggg	att
131	Gly	Val	Ala	Thr	Asp	Lys	Ser	Glu	Ala	Lys	Val	Thr	Val	Gly	Ile	
132						260				265			270			
134	tcc	gtt	aag	cca	ggc	gag	gct	goc	aag	gtt	ttc	cgt	ggc	ttg	gtt	gat
135	Ser	Asp	Lys	Pro	Gly	Glu	Ala	Ala	Lys	Val	Phe	Arg	Ala	Leu	Ala	Asp
136						275			280			285				
138	gca	gaa	atc	aac	att	gac	atg	gtt	ctg	cag	aac	gtc	tcc	tct	gtg	gaa
139	Ala	Glu	Ile	Asn	Ile	Asp	Met	Val	Leu	Gln	Asn	Val	Ser	Ser	Val	Glu
140						290			295			300				
142	gac	ggc	acc	acc	gac	atc	acg	tcc	acc	cgc	gtc	gac	ggg	cgc		960
143	Asp	Gly	Thr	Thr	Asp	Ile	Thr	Phe	Thr	Cys	Pro	Arg	Ala	Asp	Gly	Arg
144	305					310				315			320			
146	cgt	ggc	atg	gag	att	ttg	aag	aag	ctt	cag	gtt	cag	ggc	aac	tgg	acc
147	Arg	Ala	Met	Glu	Ile	Leu	Lys	Lys	Leu	Gln	Val	Gln	Gly	Asn	Trp	Thr
148						325			330			335				
150	aat	gtg	ctt	tac	gac	gac	ggc	aaa	gtc	tcc	ctc	gtg	ggt	gct		1056
151	Asn	Val	Leu	Tyr	Asp	Asp	Gln	Val	Gly	Lys	Val	Ser	Leu	Val	Gly	Ala
152						340			345			350				
154	ggc	atg	aag	tct	cac	cca	ggt	gtt	acc	gca	gag	ttc	atg	gaa	gtc	ctg
155	Gly	Met	Lys	Ser	His	Pro	Gly	Val	Thr	Ala	Glu	Met	Glu	Ala	Leu	
156						355			360			365				
158	cgc	gtt	gtc	aac	atc	gaa	ttg	att	tcc	ata	tct	gag	atc	cgc		1152
159	Arg	Asp	Val	Asn	Val	Asn	Ile	Glu	Leu	Ile	Ser	Ile	Ser	Glu	Ile	Arg
160						370			375			380				
162	att	tcc	gtg	ctg	atc	cgt	gaa	gat	gtt	ctg	gat	gtc	gtt	gca	cgt	gca

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Input Set : A:\1533 1030002 seq list.txt  
Output Set: N:\CRF3\07032001\1722441.raw

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164 385 390 395 400  
166 ttg cat gag cag ttc cag ctg ggc ggc gaa gac gaa gcc gtc gtt tat 1248  
167 Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr  
168 405 410 415  
170 gca ggc acc gga cgc taa 1266  
171 Ala Gly Thr Gly Arg  
172 420  
175 <210> SEQ ID NO: 2  
177 <211> LENGTH: 421  
179 <212> TYPE: PRT  
181 <213> ORGANISM: Corynebacterium glutamicum  
185 <400> SEQUENCE: 2  
187 Met Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala  
188 1 5 10 15  
191 Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala  
192 20 25 30  
195 Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp  
196 35 40 45  
199 Glu Leu Leu Glu Leu Ala Ala Val Asn Pro Val Pro Pro Ala Arg  
200 50 55 60  
203 Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu  
204 65 70 75 80  
207 Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr  
208 85 90 95  
211 Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg  
212 100 105 110  
215 Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly  
216 115 120 125  
219 Lys Ile Cys Ile Val Ala Gly Phe Glu Gly Val Asn Lys Glu Thr Arg  
220 130 135 140  
223 Asp Val Thr Thr Leu Gly Arg Gly Ser Asp Thr Thr Ala Val Ala  
224 145 150 155 160  
227 Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val  
228 165 170 175  
231 Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys  
232 180 185 190  
235 Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly  
236 195 200 205  
239 Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn  
240 210 215 220  
243 Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu  
244 225 230 235 240  
247 Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Ala Val Leu Thr  
248 245 250 255  
251 Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile  
252 260 265 270  
255 Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp  
256 275 280 285

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Input Set : A:\1533\_1030002 seq.list.txt

Output Set: N:\CRF3\07032001\I722441.raw

259 Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu  
 260 290 295 300  
 263 Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ala Asp Gly Arg  
 264 305 310 315 320  
 267 Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr  
 268 325 330 335 335  
 271 Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala  
 272 340 345 350  
 275 Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu  
 276 355 360 365  
 279 Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Ile Ser Glu Ile Arg  
 280 370 375 380  
 283 Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala  
 284 385 390 395 400  
 287 Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr  
 288 405 410 415  
 291 Ala Gly Thr Gly Arg  
 292 420  
 295 <210> SEQ ID NO: 3  
 297 <211> LENGTH: 1035  
 299 <212> TYPE: DNA  
 301 <213> ORGANISM: Corynebacterium glutamicum  
 305 <220> FEATURE:  
 307 <221> NAME/KEY: CDS  
 309 <222> LOCATION: (1)..(1035)  
 313 <400> SEQUENCE: 3

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316 1 5 10 15	
318 atg cgc acc ttt ttg gaa gag cgc aat ttc cca gct gac act gtt cgt	96
319 Met Arg Thr Phe Leu Glu Glu Arg Asn Phe Pro Ala Asp Thr Val Arg	
320 20 25 30	
322 ttc ttt gct tcc ccg cgt tcc gca ggc cgt aag att gaa ttc cgt ggc	144
323 Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly	
324 35 40 45	
326 acg gaa atc gag gta gaa gac att act cag gca acc gag gag tcc ctc	192
327 Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu	
328 50 55 60	
330 aag ggc atc gac gtt gcg ttg ttc tct gct gga ggc acc gct tcc aag	240
331 Lys Gly Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys	
332 65 70 75 80	
334 cag tac gct cca ctg ttt gct gct gca ggc gcg act gtt gtg gat aac	288
335 Gln Tyr Ala Pro Leu Phe Ala Ala Gly Ala Thr Val Val Asp Asn	
336 85 90 95	
338 tct tct gct tgg cgc aag gac gac gag gac gtt cca cta atc gtc tct gag	336
339 Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu	
340 100 105 110	
342 gtg aac cct tcc gac aag gat tcc ctg gtc aag ggc att att gcg aat	384
343 Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn	

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Input Set : A:\1533 1030002 seq list.txt

Output Set: N:\CRF3\07032001\I722441.raw

344	115	120	125	
346	cct aac tgc acc acc atg gct gca atg cca gtg ctg aag cca ctg cac			432
347	Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His			
348	130	135	140	
350	gat gcc gtc ggt ctt gta aag ctt cac gtt tcc tct tac cag gtc gtt			480
351	Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val			
352	145	150	155	160
354	tcc ggt tct gtc gtt gca ggt gtg gaa acc ttg gca aag cag gtc gtt			528
355	Ser Gly Ser Gly Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala			
356	165	170	175	
358	gca gtt ggc gac cac aac gtt gag ttc gtc cat gat gga cag gtc gtt			576
359	Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala			
360	180	185	190	
362	gac gca ggc gat gtc gga ctt tac gtt tcc cca atc gtc tac aac gtc			624
363	Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val			
364	195	200	205	
366	ctg ctc ttc gcc gga aac ctc gtc gat gac ggc acc ttc gaa acc gag			672
367	Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp			
368	210	215	220	
370	gaa gag cag aag ctc cgc aac gaa tcc cgc aag att ctc ggc ctc cca			720
371	Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro			
372	225	230	235	240
374	gac ctc aag gtc tca ggc acc tgc gtc cgc gtg ccg gtt ttc acc ggc			768
375	Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly			
376	245	250	255	
378	cac acg ctg acc att cac gcc gaa ttc gac aag gca atc acc gtc gag			816
379	His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Glu			
380	260	265	270	
382	cag gcg cag gag atc ttg ggt gcc gtc tca ggc gtc gag ctt gtc gac			864
383	Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Glu Leu Val Asp			
384	275	280	285	
386	gtc cca acc cca ctt gca gtc ggc ggc att gac gaa tcc ctc gtt gga			912
387	Val Pro Thr Pro Leu Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly			
388	290	295	300	
390	cgc atc cgt cag gag tcc act gtc gac gac aac cgc ggt ctg gtt ctc			960
391	Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu			
392	305	310	315	320
394	gtc gta tct ggc gat aac ctt cgc aag ggc gca gca ctg aac acc att			1008
395	Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile			
396	325	330	335	
398	cag att gtc gag ctg ctg gtt aag taa			1035
399	Gln Ile Ala Glu Leu Leu Val Lys			
400	340			
403	<210> SEQ ID NO: 4			
405	<211> LENGTH: 344			
407	<212> TYPE: PRT			
409	<213> ORGANISM: Corynebacterium glutamicum			
413	<400> SEQUENCE: 4			
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VERIFICATION SUMMARY  
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Input Set : A:\1533 1030002 seq list.txt  
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L:2055 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:23  
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